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<110> KuDOS Pharmaceuticals Limited
Jackson, Stephen P
Durocher, Daniel

<120> Screening Methods Based on FHA Domains

<130> MEWE014

<140> PCT/GB00/01024
<141> 2000-03-17

<150> GB 9906432.1
<151> 1999-03-19

<150> GB 9915075.7
<151> 1999-06-28

<160> 57

<170> PatentIn Ver. 2.1

<210> 1
<211> 56
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus

<220>

<221> SITE
<222> (1, 14, 21, 37, 53, 55)
<223> Xaa represents a hydrophobic amino acid

<220>

<221> SITE
<222> (3)
<223> Xaa is Arg or Lys

<220>

<221> SITE
<222> (4)..(13), 17, 20, 22..31, 39..46, 48, 49, 52, 54
<223> Xaa represents any amino acid

<220>

<221> SITE
<222> (15)
<223> Xaa is Ser or Gly

<220>

<221> SITE
<222> (16)
<223> Xaa is Arg or Asn

<220>

<221> SITE
<222> (18)
<223> Xaa is His or Gln

<220>
<221> SITE
<222> (32)
<223> Xaa is Ser or Thr or Gly

<220>
<221> SITE
<222> (38)
<223> Xaa is Asn or Asp

<220>
<221> SITE
<222> (47)
<223> Xaa is Leu or Ile

<220>
<221> VARIANT
<222> (4)..(13)
<223> 10 - 40 Xaa

<220>
<221> VARIANT
<222> (22)..(31)
<223> 10 - 50 Xaa

<220>
<221> VARIANT
<222> (39)..(46)
<223> 8 - 25 Xaa

<400> 1
Xaa Gly Xaa
1 5 10 15

Xaa Xaa Ala Xaa
20 25 30

Asn Gly Thr Phe Xaa
35 40 45

Xaa Gly Asp Xaa Xaa Xaa Xaa Gly
50 55

<210> 2
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
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<400> 2
Ala Pro Pro Leu Ser Gln Glu Thr Phe Ser Asp Leu Trp Lys Leu

1

5

10

15

<210> 3
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesised

<220>
<221> MOD_RES
<222> (5)
<223> PHOSPHORYLATION

<400> 3
Ala Pro Pro Leu Ser Gln Glu Thr Phe Ser Asp Leu Trp Lys Leu
1 5 10 15

<210> 4
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesised

<220>
<221> MOD_RES
<222> (8)
<223> PHOSPHORYLATION

<400> 4
Ala Pro Pro Leu Ser Gln Glu Thr Phe Ser Asp Leu Trp Lys Leu
1 5 10 15

<210> 5
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesised

<220>
<221> MOD_RES
<222> (8)
<223> PHOSPHORYLATION

<400> 5
Ala Pro Pro Leu Ala Gln Glu Thr Phe Ser Asp Leu Trp Lys Leu
1 5 10 15

<210> 6
<211> 15

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesised

<220>
<221> MOD_RES
<222> (8)
<223> PHOSPHORYLATION

<400> 6
Ala Pro Pro Leu Ser Ala Glu Thr Phe Ser Asp Leu Trp Lys Leu
1 5 10 15

<210> 7
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesised

<220>
<221> MOD_RES
<222> (8)
<223> PHOSPHORYLATION

<400> 7
Ala Pro Pro Leu Ser Gln Ala Thr Phe Ser Asp Leu Trp Lys Leu
1 5 10 15

<210> 8
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesised

<220>
<221> MOD_RES
<222> (8)
<223> PHOSPHORYLATION

<400> 8
Ala Pro Pro Leu Ser Gln Glu Thr Ala Ser Asp Leu Trp Lys Leu
1 5 10 15

<210> 9
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesised

<220>
<221> MOD_RES
<222> (8)
<223> PHOSPHORYLATION

<400> 9
Ala Pro Pro Leu Ser Gln Glu Thr Phe Ala Asp Leu Trp Lys Leu
1 5 10 15

<210> 10
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesised

<220>
<221> MOD_RES
<222> (8)
<223> PHOSPHORYLATION

<400> 10
Ala Pro Pro Leu Ser Gln Glu Thr Phe Ser Ala Leu Trp Lys Leu
1 5 10 15

<210> 11
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesised

<220>
<221> MOD_RES
<222> (6)
<223> PHOSPHORYLATION

<400> 11
Ala Leu Ala Ala Ala Thr Ala Ala Asp Ala Ala Leu
1 5 10

<210> 12
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesised

<400> 12
Ala Leu Ala Ala Ala Asp Ala Ala Asp Ala Ala Leu
1 5 10

<210> 13
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesised

<220>
<221> MOD_RES
<222> (8)
<223> PHOSPHORYLATION

<400> 13
Ala Pro Pro Leu Ser Gln Glu Ser Phe Ser Asp Leu Trp Lys Leu
1 5 10 15

<210> 14
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesised

<400> 14
Gly Gly Lys Lys Ala Thr Gln Ser Gln Glu Tyr
1 5 10

<210> 15
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesised

<220>
<221> MOD_RES
<222> (8)
<223> PHOSPHORYLATION

<400> 15
Gly Gly Lys Lys Ala Thr Gln Ser Gln Glu Tyr
1 5 10

<210> 16
<211> 87
<212> PRT
<213> *Saccharomyces cerevisiae*

<220>
<221> SITE
<222> 9..23, 43..50, 69..75
<223> Xaa is uncertain

<400> 16
Val Thr Ile Gly Arg Asn Thr Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Ile Asp Ile Asp Leu Gly Pro Ala Lys
20 25 30

Ile Val Ser Arg Lys His Ala Ala Ile Arg Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45

Xaa Xaa Glu Leu Gln Ile Phe Gly Arg Asn Gly Ala Lys Val Asn Phe
50 55 60

Arg Arg Ile Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Val Leu Gln Ser
65 70 75 80

Gly Cys Ile Ile Asp Ile Gly
85

<210> 17
<211> 90
<212> PRT
<213> *Saccharomyces cerevisiae*

<220>
<221> SITE
<222> 9..26, 46..53, 72..78
<223> Xaa is uncertain

<400> 17
Val Ser Ile Gly Arg Asn Thr Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Asn Ile Asp Leu Gly
20 25 30

Pro Ala Lys Val Val Ser Arg Lys His Ala Ile Ile Lys Xaa Xaa Xaa
35 40 45

Xaa Xaa Xaa Xaa Xaa Glu Leu His Ile Leu Gly Arg Asn Gly Ala Lys
50 55 60

Val Asn Phe Gln Arg Thr His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile Arg
65 70 75 80

Leu Ser Ser Gly Thr Leu Leu Asp Ile Gly
85 90

<210> 18
<211> 105
<212> PRT
<213> *Saccharomyces cerevisiae*

<220>
<221> SITE
<222> 29..68
<223> Xaa is uncertain

<400> 18
Ile Thr Val Gly Arg Asn Ser Ser Gln Cys Asp Val Ala Leu Cys Lys
1 5 10 15

Asn Lys Phe Ile Ser Arg Val His Ala Ser Ile Thr Xaa Xaa Xaa Xaa
20 25 30

Xaa
35 40 45

Xaa
50 55 60

Xaa Xaa Xaa Ala Tyr Arg Leu Val Pro Arg Phe Ser Asn Glu Lys
65 70 75 80

Cys Val Lys Glu Ile Gln Asp Glu Gly Gly Phe Ile Asn Phe Thr Leu
85 90 95

Glu Glu Gly Asp Thr Val Tyr Met Thr
100 105

<210> 19
<211> 67
<212> PRT
<213> *Saccharomyces cerevisiae*

<220>
<221> SITE
<222> 28..33
<223> Xaa is uncertain

<400> 19
Trp Thr Phe Gly Arg Asn Pro Ala Cys Asp Tyr His Leu Gly Asn Ile
1 5 10 15

Ser Arg Leu Ser Asn Lys His Phe Gln Ile Leu Xaa Xaa Xaa Xaa
20 25 30

Xaa Leu Leu Asn Asp Ile Ser Thr Asn Gly Thr Trp Leu Asn Gly Gln
35 40 45

Lys Val Glu Lys Asn Ser Asn Gln Leu Leu Ser Gln Gly Asp Glu Ile
50 55 60

Thr Val Gly
65

<210> 20
<211> 73
<212> PRT
<213> *Schizosaccharomyces pombe*

<220>
<221> SITE
<222> 27..39
<223> Xaa is uncertain

<400> 20
Trp Gly Phe Gly Arg His Lys Ser Cys Glu Val Val Leu Asn Gly Pro
1 5 10 15

Arg Val Ser Asn Phe His Phe Glu Ile Tyr Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Phe Leu His Asp Ile Ser Ser Asn Gly
35 40 45

Thr Phe Leu Asn Phe Glu Arg Leu Ala Lys Asn Ser Arg Thr Ile Leu
50 55 60

Ser Asn Gly Asp Glu Ile Arg Ile Gly
65 70

<210> 21
<211> 65
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<221> SITE
<222> 27..32
<223> Xaa is uncertain

<400> 21
Thr Arg Ile Gly Arg Leu His Asp Asn Asp Ile Val Leu Asp Ser Ala
1 5 10 15

Asn Val Ser Arg His His Ala Val Ile Val Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Val Ile Asn Asp Leu Arg Ser Ser Asn Gly Val His Val Gln His Glu
35 40 45

Arg Ile Arg Ser Ala Val Thr Leu Asn Asp Gly Asp His Ile Arg Ile
50 55 60

Cys
65

<210> 22
<211> 64
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<221> SITE
<222> 27..32
<223> Xaa is uncertain

<400> 22
Val Arg Ile Gly Arg Ala Asn Asp Asn Asp Ile Val Ile Pro Glu Val
1 5 10 15

Leu Ala Ser Arg His His Ala Thr Leu Val Xaa Xaa Xaa Xaa Xaa

20

25

30

Glu Ile Arg Asp Asn Arg Ser Ile Asn Gly Thr Phe Val Asn Gly Ala
35 40 45

Arg Val Asp Ala Ala Leu Leu His Asp Gly Asp Val Val Thr Ile Gly
50 55 60

<210> 23

<211> 89

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> SITE

<222> 9..25, 48..55

<223> Xaa is uncertain

<400> 23

Leu Lys Leu Gly Arg Pro Val Thr Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Val Arg Pro Asp Asn Gly
20 25 30

Asn Phe Asp Ser Arg Val Leu Ser Arg Asn His Ala Cys Leu Ser Xaa
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Ile Arg Asp Leu Lys Ser Ser Asn
50 55 60

Gly Thr Phe Val Asn Gly Val Lys Ile Arg Gln Asn Asp Val Glu Leu
65 70 75 80

Lys Val Gly Asp Thr Val Asp Leu Gly
85

<210> 24

<211> 94

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> SITE

<222> 9..30, 53..60

<223> Xaa is uncertain

<400> 24

Leu Lys Leu Gly Arg Pro Val Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Gln Val
20 25 30

Arg Ser Asp Asn Gly Asn Phe Asp Ser Arg Val Leu Ser Arg Asn His
35 40 45

Ala Leu Leu Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Ile Arg Asp
50 55 60

Leu Lys Ser Ser Asn Gly Thr Phe Ile Asn Gly Gln Arg Ile Gly Ser
65 70 75 80

Asn Asp Val Glu Ile Lys Val Gly Asp Val Ile Asp Leu Gly
85 90

<210> 25

<211> 85

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> SITE

<222> 9..17, 40..46, 66..73

<223> Xaa is uncertain

<400> 25

Ile Ile Ile Gly Arg Tyr Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Pro Asp Gln Tyr His Pro Val Val Phe Lys Ser Lys Val Ile Ser
20 25 30

Arg Thr His Gly Cys Phe Lys Xaa Xaa Xaa Xaa Xaa Xaa Phe Leu
35 40 45

Lys Asp Val Lys Ser Ser Gly Thr Phe Leu Asn His Gln Arg Leu
50 55 60

Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Leu Leu His Asp Gly Asp
65 70 75 80

Ile Ile Gln Leu Gly
85

<210> 26

<211> 85

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> SITE

<222> 9..17, 40..46, 66..73

<223> Xaa is uncertain

<400> 26

Leu Val Ile Gly Arg Tyr Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Pro Glu Gln Tyr His Pro Val Val Phe Lys Ser Lys Val Val Ser
20 25 30

Arg Thr His Gly Cys Phe Lys Xaa Xaa Xaa Xaa Xaa Xaa Tyr Ile
35 40 45

Lys Asp Val Lys Ser Ser Ser Gly Thr Phe Leu Asn His Gln Arg Leu
50 55 60

Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Pro Leu Arg Asp Gly Asp
65 70 75 80

Ile Leu Gln Leu Gly
85

<210> 27

<211> 78

<212> PRT

<213> Schizosaccharomyces pombe

<220>

<221> SITE

<222> 34..39, 59..66

<223> Xaa is uncertain

<400> 27

Ile Tyr Ile Gly Arg Tyr Thr Glu Arg Tyr Asn Gly Gly Asp Val Ser
1 5 10 15

Ala Ile Val Phe Arg Ser Lys Val Val Ser Arg Arg His Ala Gln Ile
20 25 30

Phe Xaa Xaa Xaa Xaa Xaa Xaa Tyr Ile Gln Asp Met Gly Ser Ser Ser
35 40 45

Gly Thr Phe Leu Asn His Val Arg Leu Ser Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60

Xaa Xaa Tyr Pro Ile Ser Asn Asn Asp Ile Leu Gln Leu Gly
65 70 75

<210> 28

<211> 64

<212> PRT

<213> Mycobacterium tuberculosis

<220>

<221> SITE

<222> 27..32

<223> Xaa is uncertain

<400> 28

Asn Ile Ile Gly Arg Gly Gln Asp Ala Gln Phe Arg Leu Pro Asp Thr
1 5 10 15

Gly Val Ser Arg Arg His Leu Glu Ile Arg Xaa Xaa Xaa Xaa Xaa
20 25 30

Leu Leu Ala Asp Leu Asn Ser Thr Asn Gly Thr Thr Val Asn Asn Ala
35 40 45

Pro Val Gln Glu Trp Gln Leu Ala Asp Gly Asp Val Ile Arg Leu Gly
50 55 60

<210> 29
<211> 66
<212> PRT
<213> Anabaena sp.

<220>
<221> SITE
<222> 27..33
<223> Xaa is uncertain

<400> 29
Phe Thr Ile Gly Arg Leu Pro Glu Cys Asn Leu Tyr Leu Pro Phe Ala
1 5 10 15

Gly Val Ser Arg Lys His Ala Gln Leu Val Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Ile Ile Glu Asp Leu Gly Ser Lys Asn Gly Thr Gln Val Asn Gln
35 40 45

Ser Ile Val Ser His Pro Arg Gln Leu Gln His Gly Asp Val Ile Trp
50 55 60

Leu Gly
65

<210> 30
<211> 72
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> SITE
<222> 31..38
<223> Xaa is uncertain

<400> 30
Ala Ile Ile Gly Arg Arg Ser Glu Asn Asp Phe Ser His Lys Val Asp
1 5 10 15

Val Asn Leu Gly Pro Ile Ser Arg Arg His Ala Gln Ile Phe Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Glu Leu Ser Ile Ile Gly Lys Asn Gly Ala
35 40 45

Phe Val Asp Asp Ile Phe Val Glu Lys Gly Asn Thr Val Pro Leu Arg
50 55 60

Asn Lys Thr Lys Ile Gin Ile Gly
65 70

<210> 31
<211> 64
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<221> SITE
<222> 27..32
<223> Xaa is uncertain

<400> 31

Thr	Ser	Ala	Gly	Arg	His	Pro	Asp	Ser	Asp	Ile	Phe	Leu	Asp	Asp	Val
1										10					15

Thr Val Ser Arg Arg His Ala Glu Phe Arg Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Asn Val Val Asp Val Gly Ser Leu Asn Gly Thr Tyr Val Asn Arg Glu
35 40 45

Pro Val Asp Ser Ala Val Leu Ala Asn Gly Asp Glu Val Gln Ile Gly
50 55 60

<210> 32
<211> 64
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<221> SITE
<222> 27..31
<223> Xaa is uncertain

<400> 32

Val	Leu	Ile	Gly	Arg	Ala	Asp	Asp	Ser	Thr	Leu	Val	Leu	Thr	Asp	Asp
1									10					15	

Tyr Ala Ser Thr Arg His Ala Arg Leu Ser Xaa Xaa Xaa Xaa Xaa Tyr
20 25 30

Val Glu Asp Leu Gly Ser Thr Asn Gly Thr Tyr Leu Asp Arg Ala Lys
35 40 45

Val Thr Thr Ala Val Arg Val Pro Ile Gly Thr Pro Val Arg Ile Gly
50 55 60

<210> 33
<211> 73
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> SITE
<222> 27..38
<223> Xaa is uncertain

<400> 33
Thr Thr Ile Gly Arg Ser Arg Ser Cys Asp Val Ile Leu Ser Glu Pro
1 5 10 15

Asp Ile Ser Thr Phe His Ala Glu Phe His Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Leu Ile Asn Val Ile Asp Lys Ser Arg Asn
35 40 45

Gly Thr Phe Ile Asn Gly Asn Arg Leu Val Lys Lys Asp Tyr Ile Leu
50 55 60

Lys Asn Gly Asp Arg Ile Val Phe Gly
65 70

<210> 34
<211> 109
<212> PRT
<213> *Saccharomyces cerevisiae*

<220>
<221> SITE
<222> 29..66, 91..97
<223> Xaa is uncertain

<400> 34
Leu Ala Ile Gly Arg Lys Lys Ser Val Cys Asn Ile Ile Leu Pro Cys
1 5 10 15

Arg Lys Asn Ile Ser Arg Gln His Ala Phe Ile Ser Xaa Xaa Xaa Xaa
20 25 30

Xaa
35 40 45

Xaa
50 55 60

Xaa Xaa Phe Tyr Lys Leu Val Ala Glu Glu Pro Leu Thr Ser Gln Asn
65 70 75 80

Thr Lys Gln Ser His Gly Lys Thr Leu Gln Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95

Xaa Phe Val Leu Ala Lys Gly Glu Thr Val Thr Phe Pro
100 105

<210> 35
<211> 74
<212> PRT
<213> *Anabaena* sp.

<220>
<221> SITE
<222> 34..39
<223> Xaa is uncertain

<400> 35
Val His Ile Gly Lys Pro Asn Asp Arg Ile Pro Pro Asp Val Asp Val
1 5 10 15

Ser Gly Phe Ala Asn Ser Glu Ile Val Ser Arg Val His Ala Asp Ile
20 25 30

Arg Xaa Xaa Xaa Xaa Xaa Tyr Ile Glu Asp Val Gly Ser Ser Asn
35 40 45

Gly Thr Tyr Ile Asn Asn Leu Pro Leu Leu Pro Gly Asn Arg His Arg
50 55 60

Leu Arg Pro Gly Asp Arg Ile Ser Leu Gly
65 70

<210> 36
<211> 66
<212> PRT
<213> Synechocystis sp.

<220>
<221> SITE
<222> 27..33
<223> Xaa is uncertain

<400> 36
Trp Thr Val Gly Arg Ser Gln Asp Asn Asp Leu Val Ile Arg Asp Asn
1 5 10 15

Cys Ile Ser Arg Asn His Ala Ile Leu Gln Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Leu Leu Ile Asp Leu Gly Ser Arg Asn Gly Thr Phe Val Asn Gly
35 40 45

Arg Arg Val Ser Val Pro Ile Ala Ile Gln Asp Gln Asp Lys Ile Thr
50 55 60

Phe Gly
65

<210> 37
<211> 77
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> 27..43
<223> Xaa is uncertain

<400> 37
Tyr Val Val Gly Arg Lys Asn Cys Ala Ile Leu Ile Glu Asn Asp Gln
1 5 10 15

Ser Ile Ser Arg Asn His Ala Val Leu Thr Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Thr Leu Lys Asp Asn
35 40 45

Ser Lys Tyr Gly Thr Phe Val Asn Glu Glu Lys Met Gln Asn Gly Phe
50 55 60

Ser Arg Thr Leu Lys Ser Gly Asp Gly Ile Thr Phe Gly
65 70 75

<210> 38

<211> 78

<212> PRT

<213> Drosophila melanogaster

<220>

<221> SITE

<222> 35..44

<223> Xaa is uncertain

<400> 38

Phe Thr Ala Gly Arg Gly Glu Ala Asn Asp Leu Ile Leu Thr Leu Asn
1 5 10 15

Asp Leu Pro Glu Lys Ile Leu Thr Arg Ile Ser Lys Val His Phe Ile
20 25 30

Ile Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Ile Gln Asp
35 40 45

Leu Ser Arg Asn Gly Thr Phe Val Asn Asn Glu Lys Ile Gly Thr Asn
50 55 60

Arg Met Arg Ile Leu Lys Asn Asp Asp Val Ile Ser Leu Ser
65 70 75

<210> 39

<211> 80

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> 36..46

<223> Xaa is uncertain

<400> 39

Tyr Trp Phe Gly Arg Asp Lys Ser Cys Glu Tyr Cys Phe Asp Glu Pro
1 5 10 15

Leu Leu Lys Arg Thr Asp Lys Tyr Arg Thr Tyr Ser Lys Lys His Phe

20

25

30

Arg Ile Phe Xaa Tyr Ile
35 40 45

Glu Asp His Ser Gly Asn Gly Thr Phe Val Asn Thr Glu Leu Val Gly
50 55 60

Lys Gly Lys Arg Arg Pro Leu Asn Asn Asn Ser Glu Ile Ala Leu Ser
65 70 75 80

<210> 40

<211> 71

<212> PRT

<213> Mus musculus

<220>

<221> SITE

<222> 31..36

<223> Xaa is uncertain

<400> 40

Val Thr Ile Gly Arg Asn Ser Ser Gln Gly Ser Val Asp Leu Ser Met
1 5 10 15

Gly Leu Ser Ser Phe Ile Ser Arg Arg His Leu Gln Leu Ser Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Tyr Leu Arg Cys Leu Gly Lys Asn Gly Val Phe Val
35 40 45

Asp Gly Ala Phe Gln Arg Arg Gly Ala Pro Ala Leu Gln Leu Pro Gln
50 55 60

Gln Cys Thr Phe Arg Phe Pro
65 70

<210> 41

<211> 67

<212> PRT

<213> Synechocystis sp.

<220>

<221> SITE

<222> 27..35

<223> Xaa is uncertain

<400> 41

Tyr Phe Leu Gly Arg Ser Ser Ser Cys Asp Ile Gln Leu Gln Asn Pro
1 5 10 15

Leu Val Ser Gln Thr His Cys Ser Leu Arg Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Phe Ile Arg Asp Glu Gly Ser Ser Asn Gly Ile Tyr Leu
35 40 45

Gln Arg Arg Arg Leu Lys Ser Tyr Arg Leu Gln His Gly Asp Glu Ile
50 55 60

Thr Leu Gly
65

<210> 42
<211> 73
<212> PRT
<213> *Saccharomyces cerevisiae*

<220>
<221> SITE
<222> 28..39
<223> Xaa is uncertain

<400> 42
Val Lys Val Gly Arg Asn Asp Lys Glu Cys Gln Leu Val Leu Thr Asn
1 5 10 15

Pro Ser Ile Ser Ser Val His Cys Val Phe Trp Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Tyr Val Lys Asp Cys Ser Leu Asn Gly
35 40 45

Thr Tyr Leu Asn Gly Leu Leu Lys Arg Asp Lys Thr Tyr Leu Leu
50 55 60

Lys His Cys Asp Val Ile Glu Leu Ser
65 70

<210> 43
<211> 77
<212> PRT
<213> *Arabidopsis thaliana*

<220>
<221> SITE
<222> 27..34, 54..65
<223> Xaa is uncertain

<400> 43
Val Lys Leu Gly Arg Val Ser Pro Ser Asp Leu Ala Leu Lys Asp Ser
1 5 10 15

Glu Val Ser Gly Lys His Ala Gln Ile Thr Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Glu Leu Val Asp Met Gly Ser Leu Asn Gly Thr Leu Val Asn
35 40 45

Ser His Ser Ile Ser Xaa
50 55 60

Xaa Val Glu Leu Ala Ser Asp Asp Ile Ile Thr Leu Gly
65 70 75

<210> 44
<211> 65
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> 27..32
<223> Xaa is uncertain

<400> 44
Cys Leu Phe Gly Arg Gly Ile Glu Cys Asp Ile Arg Ile Gln Leu Pro
1 5 10 15

Val Val Ser Lys Gln His Cys Lys Ile Glu Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Ile Leu His Asn Phe Ser Ser Thr Asn Pro Thr Gln Val Asn Gly Ser
35 40 45

Val Ile Asp Glu Pro Val Arg Leu Lys His Gly Asp Val Ile Thr Ile
50 55 60

Ile
65

<210> 45
<211> 75
<212> PRT
<213> Caenorhabditis elegans

<220>
<221> SITE
<222> 28..40
<223> Xaa is uncertain

<400> 45
Val Val Ile Gly Arg Ile Lys Pro Gly Cys Asp Leu Leu Met Glu His
1 5 10 15

Pro Ser Ile Ser Arg Tyr His Cys Ile Leu Gln Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa His Ile Phe Glu Leu Gly Ser Thr
35 40 45

His Gly Ser Arg Met Asn Lys Lys Arg Leu Pro Pro Lys Gln Tyr Ile
50 55 60

Arg Thr Arg Val Gly Phe Ile Phe Gln Phe Gly
65 70 75

<210> 46

<211> 88
<212> PRT
<213> *Saccharomyces cerevisiae*

<220>
<221> SITE
<222> 36..54
<223> Xaa is uncertain

<400> 46
Lys Thr Ile Gly Arg Ser Ser Ser Phe Asp Gln Asn Ser Leu Cys Lys
1 5 10 15

Pro Tyr Asn Leu Tyr Phe Asp Glu Pro Glu Leu Ser Arg Gln His Ala
20 25 30

Val Leu Cys Xaa
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Cys Ile Arg Asp Leu Asn Asn Lys Thr Gly
50 55 60

Thr Val Asn Leu Val Ser Asp Gly Pro Asn Asp Glu Ile Asp Leu Lys
65 70 75 80

Asn Gly Asp Ala Phe Gly Leu Ile
85

<210> 47
<211> 81
<212> PRT
<213> *Saccharomyces cerevisiae*

<220>
<221> SITE
<222> 27..42
<223> Xaa is uncertain

<400> 47
Phe Phe Ile Gly Arg Ser Glu Asp Cys Asn Cys Lys Ile Glu Asp Asn
1 5 10 15

Arg Leu Ser Arg Val His Cys Phe Ile Phe Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Leu Asp Asp Ile Trp
35 40 45

Tyr Cys His Thr Gly Thr Asn Val Ser Tyr Leu Asn Asn Arg Met
50 55 60

Ile Gln Gly Thr Lys Phe Leu Leu Gln Asp Gly Asp Glu Ile Lys Ile
65 70 75 80

Ile

<210> 48
<211> 86
<212> PRT
<213> *Saccharomyces cerevisiae*

<220>
<221> SITE
<222> 9..23, 42..51
<223> Xaa is uncertain

<400> 48
Tyr Leu Val Gly Arg Glu Leu Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Ala Asp Ile Gly Ile Pro Glu Glu Thr
20 25 30

Ser Ser Lys Gln His Cys Val Ile Gln Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45

Xaa Xaa Xaa Tyr Val Met Asp Leu Asp Ser Ser Asn Gly Thr Cys Leu
50 55 60

Asn Asn Val Val Ile Pro Gly Ala Arg Tyr Ile Glu Leu Arg Ser Gly
65 70 75 80

Asp Val Leu Thr Leu Ser
85

<210> 49
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Linker

<400> 49
Ser Gly Ser Gly
1

<210> 50
<211> 9
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Sequence source
uncertain

<220>
<221> MOD_RES
<222> (4)
<223> PHOSPHORYLATION

<400> 50
Gly Asp Gly Tyr Glu Glu Ile Pro Ile

<210> 51
<211> 12
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Sequence source
uncertain

<220>
<221> MOD_RES
<222> (10)
<223> PHOSPHORYLATION

<400> 51
Val Pro Val Ser Val Asp Asn Pro Thr Tyr Leu Leu
1 5 10

<210> 52
<211> 11
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Sequence source
uncertain

<400> 52
Pro Val Arg Gln Val Pro Leu Arg Pro Met Thr
1 5 10

<210> 53
<211> 15
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Sequence source
uncertain

<220>
<221> MOD_RES
<222> (9)
<223> PHOSPHORYLATION

<400> 53
Leu Ser Gln Arg Gln Arg Ser Thr Ser Thr Pro Asn Val His Ala
1 5 10 15

<210> 54
<211> 11
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Sequence source
uncertain

<220>
<221> MOD_RES
<222> (5)
<223> PHOSPHORYLATION

<400> 54
Lys Gly Gly Gln Tyr Glu Glu Ile Pro Ile Pro
1 5 10

<210> 55
<211> 7
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Sequence source
uncertain

<220>
<221> MOD_RES
<222> (6)
<223> PHOSPHORYLATION

<400> 55
Ala Tyr Ile Gly Pro Tyr Leu
1 5

<210> 56
<211> 10
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Sequence source
uncertain

<220>
<221> MOD_RES
<222> (5)
<223> PHOSPHORYLATION

<400> 56
Glu Gln Pro Leu Thr Pro Val Thr Asp Leu
1 5 10

<210> 57
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesised

<220>
<221> SITE
<222> (9)..(11)
<223> Xaa=fully degenerate for all amino acid residues,
except cysteine

<220>
<221> MOD_RES
<222> (8)
<223> PHOSPHORYLATION in T(P) peptide

<400> 57
Ser Gly Ser Tyr Ser Gln Glu Thr Xaa Xaa Xaa Leu Leu
1 5 10